

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:07:10 : Search time 19.51 Seconds
(without alignments)
2077.133 Million cell updates/sec

Title: US-09-911-513-2

Perfect score: 2758

Sequence: 1 MKRDHHHHQDKKTKMMNEE.....MLGWHTRPLIATSANKLSTN 532

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2747.5	99.6	533	2 H86282	protein F10B6.34 [
2	2185.5	79.2	587	2 D84426	hypothetical prote
3	1587	57.5	511	2 G9688	hypothetical prote
4	1490	54.0	523	2 T51475	RGA-like protein -
5	602.5	21.8	653	2 T47581	SCARECROW1 - Arabi
6	598.5	21.7	653	2 T51244	SCARECROW protein
7	588.5	21.3	658	2 D96656	hypothetical prote
8	565.5	20.5	482	2 E96540	hypothetical prote
9	564	20.4	413	2 G84462	probable SCARECROW
10	562.5	20.4	526	2 E96542	scarecrow-like pro
11	531.5	19.3	313	2 T51242	Scil protein [impo
12	506.5	18.4	306	2 T51236	scarecrow-like pro
13	487.5	17.7	593	2 E86347	hypothetical prote
14	453.5	16.4	808	2 T51232	scarecrow-like pro
15	451.5	16.4	352	2 T51234	scarecrow-like pro
16	440	16.0	1336	2 T02736	probable SCARECROW
17	431	15.6	284	2 T51241	scarecrow-like pro
18	429	15.6	375	2 C71441	probable SCARECROW
19	428	15.5	583	2 T45597	scarecrow-like pro
20	422.5	15.3	542	2 T46142	scarecrow-like 7 (
21	412	14.9	325	2 T51235	scarecrow-like pro
22	407	14.8	718	2 T02531	probable SCARECROW
23	393.5	14.3	531	2 T04722	hypothetical prote
24	389.5	14.1	573	2 T51239	scarecrow-like pro
25	378.5	13.7	483	2 T10552	hypothetical prote
26	336	12.2	558	2 T01343	hypothetical prote
27	335.5	12.2	378	2 T51237	scarecrow-like pro
28	326	11.8	640	2 B84867	probable SCARECROW
29	320.5	11.6	410	2 T45848	hypothetical prote

RESULT 1

H86282

protein F10B6.34 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: H86282

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H86282

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-533 <STO>

A:Cross-references: GB:AE005172; MID:g8778219; PIDN:AAF79228.1; GSPDB:GN00141

C:Genetics:

A:Gene: F10B6.34

A:Map position: 1

Query Match 99.6%; Score 2747.5; DB 2; Length 533;
Best Local Similarity 99.8%; Pred. No. 7.9e-197;
Matches 532; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MKRD-HHHHHQDKKTKMMNEEDGNGMDLLAVLGKYKRSSEMADVAOKLEQVMMNSV 59

Db 1 MKRDHHHHQDKKTKMMNEEDGNGMDLLAVLGKYKRSSEMADVAOKLEQVMMNSV 60

Qy 60 QEDDLSQLATETVHYNPAELYTLWDSMLTDLNPPSSNAYDYDKAIPGDAINQFAIDSAS 119

Db 61 QEDDLSQLATETVHYNPAELYTLWDSMLTDLNPPSSNAYDYDKAIPGDAINQFAIDSAS 120

Qy 120 SSNOGGGGDTVTNNKRLKCSNGVETTTATAESTRHVVLVDSQENGRVRLVHALLACAEV 179

Db 121 SSNOGGGGDTVTNNKRLKCSNGVETTTATAESTRHVVLVDSQENGRVRLVHALLACAEV 180

Qy 180 QKENLTVAEALVKGIFLAVSQIGAMRKVATYFAELARRIYRLSPSPDIDHLSLDTLQ 239

Db 181 QKENLTVAEALVKGIFLAVSQIGAMRKVATYFAELARRIYRLSPSPDIDHLSLDTLQ 240

Qy 240 MHFVETCPYLKFAHFTANQAILAEAFQGGKRVHVDFDSMSQGLQWPAALMALRPGGPPV 299

Db 241 MHFVETCPYLKFAHFTANQAILAEAFQGGKRVHVDFDSMSQGLQWPAALMALRPGGPPV 300

Qy 300 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSEI 359

ALIGNMENTS

30	306.5	11.1	623	2	T47874
31	272	9.9	486	2	E85433
32	225	8.2	205	2	T51233
33	185	6.7	133	2	T51240
34	183	6.6	261	2	T51243
35	118	4.3	9376	2	T14593
36	116.5	4.2	3971	2	T44806
37	112.5	4.1	772	2	A55004
38	110.5	4.0	664	2	S60062
39	108	3.9	275	2	T04480
40	107	3.9	112	2	T51238
41	107	3.9	1158	2	T43519
42	106.5	3.9	673	2	T47905
43	106.5	3.9	1420	2	S54471
44	106	3.8	1829	2	T26135
45	106	3.8	3206	1	GNVSPV

scarecrow-like pro
SCARECROW-like pro
scarecrow-like pro
scarecrow-like pro
Scil protein [impo
syringomycin synth
mycosubtilin synth
transcription fact
hevin precursor -
acyl-CoA oxidase h
scarecrow-like pro
condensin complex
hypothetical prote
probable membrane
hypothetical prote
genome polyprotein

Db 301 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLADSMLELRPSEI 360
Qy 360 ESVAVNSVFELHKLGRPGATDKVLGVVNOIKPEFTVVEQESHNHNSPIFLDRFTESLHY 419
Db 361 ESVAVNSVFELHKLGRPGATDKVLGVVNOIKPEFTVVEQESHNHNSPIFLDRFTESLHY 420
Qy 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
Db 421 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 480
Qy 480 AHIGSNAPKQASMLLALFNGEGYRVESDGLMLGWHTRPLIATSAWKLSTN 532
Db 481 AHIGSNAPKQASMLLALFNGEGYRVESDGLMLGWHTRPLIATSAWKLSTN 533
RESULT 2
D84426
hypothetical protein At2g01570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84426
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:2008348
A:Accession: D84426
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <STO>
A:Cross-references: GB:AE002093; NID:g3785986; PIDN:AAC67333.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g01570
A:Map position: 2

Query Match 79.2%; Score 2185.5; DB 2; Length 587;
Best Local Similarity 74.3%; Pred. No. 6.8e-155;
Matches 440; Conservative 39; Mismatches 44; Indels 69; Gaps 9;
Qy 1 MKRDHHH-----UH-----QDKTMMNEEDDNGM-DELLAVLGKYKVRSEMA 43
Db 1 MKRDHHHFOGRLSHNGTSSSSSSISDKMMVMKKEEDGGNMDDELLAVLGKYKVRSEMA 60
Qy 44 DVAOKLEQLEVMNSVQEDDLSQATETVHYNPAELYTWLDSMLTDLNPP-----SSN--- 96
Db 61 EVALKLEQLETMNSVQEDGLSHLATDTVHYNPSLEYSLWLDNMLSELNPPPLPASSNGLD 120
Qy 97 -----AEYDLKAIPGDAILNOFAIDSSASSNSQGGGDTYTNKRLK-CSN-- 140
Db 121 PVLPSPEICGFPASDYDLKVPIGNAIYQFPADSSSSN-----NONKRLKSCSPD 172
Qy 141 -----GVV-----ETTATAESTHRVVLVDSQENGVRLVHALLACAEV 179
Db 173 SWTSTGTGIGVIGTITVTITTTTAAGESTRVLVDSQENGVRLVHALLACAEAI 232
Qy 180 QKENLTVAEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPQSPIDHLSLSDTLQ 239
Db 233 QONNLTAEALVKOIGCLAVSQAGAMRKVATYFAEALARRIYRLSPQONQIDHCLSDTLQ 292
Qy 240 MHFYETCPYLKFAHTANQALAEAFQGGKRVHVIDFSMSQGLQWALMALALRPGPPV 299
Db 293 MHFYETCPYLKFAHTANQALAEAFEGKRVHVIDFSMNQGLQWALMALALRPGPPT 352
Qy 300 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLADSMLELRPSEI 359
Db 353 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLADSMLELRPSEI 412
Qy 360 ESVAVNSVFELHKLGRPGATDKVLGVVNOIKPEFTVVEQESHNHNSPIFLDRFTESLHY 419
Db 413 EAVAVNSVFELHKLGRPGGTEKVLGVVVKQIKPVITVVEQESHNHNGPVFLDRFTESLHY 472

Qy 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
Db 473 YSTLFDLSLEGVPSQDKVMSEVYLGKQICNLVACDGPDRVERHETLSQWNGRFGSSGLAP 532
Qy 480 AHIGSNAPKQASMLLALFNGEGYRVESDGLMLGWHTRPLIATSAWKLST 531
Db 533 AHLGSAFQASMLLSVFNQSGYRVESNGCLMLGWHTRPLITTSWKLST 584
RESULT 3
G96688
hypothetical protein T27F4.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96688
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96688
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <STO>
A:Cross-references: GB:AE005173; NID:gl0092507; PIDN:AAG12907.1; GSPDB:GN00141
C:Genetics:
A:Gene: T27F4.10
A:Map position: 1

Query Match 57.5%; Score 1587; DB 2; Length 511;
Best Local Similarity 59.0%; Pred. No. 2.2e-110;
Matches 319; Conservative 74; Mismatches 104; Indels 44; Gaps 9;
Qy 1 MKRDHHHHOD-----KKTMMNEEDDNGMDDELLAVLGKYKVRSEMDVAKLEQLEVM 55
Db 1 MKREHNHRESSAGEGSSMTTVIKKEAAGVDLVLVGLVKVRSDMDVAHKLQLEVM 60
Qy 56 MSNVQEDDLSQATETVHYNPAELYTWLDSMLTDLNPP-----PSSNAEYDLKAIPGDAILN 111
Db 61 LG----DGISNLSDETIVHYNPSDLGWSVMSLSLDLPTRIQEKPDSEYDLRAIPGSAYVP 116
Qy 112 OFAIDSASSNSQGGGDTYTT--NKRLKCSNGVETTTTATAESTHRVVLVDSQENGVRLV 169
Db 117 R-----DEHVTRRSKRTRIESEL-----SSTRSVVVLDSQETGVRLV 153
Qy 170 HALLACAEAVOKENLTVAEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPQSP 229
Db 154 HALLACAEAVOONNLKADALVKHGLASSQAGAMRKVATYFAEGLARRIYRIYRPDDV 213
Qy 230 IDHLSLSDTLQMHFYETCPYLKFAHTANQALAEAFQGGKRVHVIDFSMSQGLQWALMAQ 289
Db 214 ALSFSFDTLQHFYESCYPYLFKAHTANQALAEAFATAEKVHVIDGLNHNGLQWALQIA 273
Qy 290 LALRPGPPVFLTGIGPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLDA 349
Db 274 LALRPGPPDFRLTGIGYSLTD----IQEVGKWLQGLASTIGVNFESKIALNLSDLKP 329
Qy 350 SMLELRPSEIESVAVNSVFLHKLGRPGATDKVLGVVNOIKPEFTVVEQESHNHNSPIF 409
Db 330 EMLDIRPG-LESAVNSVFLHRLLAHPGSDIKFLSTIKSRPDIMTVVEQANNGTVF 388
Qy 410 LDRFTESLHYSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWR 469
Db 389 LDRFTESLHYSSFLSFLSLEGPSPS-QDRVMSSELFLOQLINLVACEGEDRVERHETLNQWR 447

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzilio, R.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719
A:Accession: E96540

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-482 <STO>
A:Cross-references: GB:AE005173; NID:g9454566; PIDN:AAF87889.1; GSPDB:GN00141
C:Genetics:
A:Gene: F17J6.12
A:Map position: 1

Query Match 20.5%; Score 565.5; DB 2; Length 482;
Best Local Similarity 31.7%; Pred. No. 2.5e-34;
Matches 145; Conservative 72; Mismatches 156; Indels 85; Gaps 11;
Qy 147 TATAESTRHVVLD--SOENGVRVLHALLACAEAVQKENLTVAEALVKQIGFLAVSQIGA 204
Db 31 TLLASSPFHCLKDLKPEERGLYLHLITCANHVASSGLQANAAALQSLHSLASPGDGT 90
Qy 205 MRKVATYFAEALARI-----YRLSPSQPIDHSLDITLQMH--FYETCPYLKFAHFT 255
Db 91 MORTAAYFTEALANRLKSWFGLYKALNATQRTNNVSEEHVRRLLFFEMFPIKVSYLL 150
Qy 256 ANOATLEAFOGKKRVHVTDFSMOSQLOWPALMOALALRPGPPVPRLTGIGPPAPDNFDY 315
Db 151 TNRAILEAMEGKVVHVIDLDAEPAQWLALQAFNSRPEGPPHURITGV-----HHQKEV 206
Qy 316 LHEVGCKLAHLAEATHVEFEYRGFVANTLADLASMLE-LRPSEIESVAVNSVFELKLL 374
Db 207 LEQMAHRLIEAEKLDIPFQNPVSR---LDCLNVQLRVKVTGEALAVSVLQLHTFL 262
Qy 375 G----- 375
Db 263 ASDDDLKRNKALRQNNPNSGVLDQRLVLMHSGSAAEARENDMSNNNGSPSGDSASSLP 322
Qy 376 --RPGADKVLGVVNOIKPEIFTVVEQSNHNSPIFLDRFTESLHYSTLFDLSLE-GVP- 431
Db 323 LPSSGRTDSFLNAGLWGLPKVWVTEQDSHGNGSTLMERLESLLTYAALFDCLETKVPR 382
Qy 432 SGQDKVMSEVYL-GKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAPKQA 490
Db 383 TSQRIKVEKMLFGEIEKNIISCEGFERRERHEKLEKWSRIDLAGFCNVPLSYAMLQA 442
Qy 491 SMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSAWK 528
Db 443 RRLIQ-GCGFGDRIKEESGCAVICQWRPLYSVAWR 479
RESULT 9
G84462
probable SCARECROW gene regulator [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84462
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-413 <STO>
A:Cross-references: GB:AE002093; NID:g4585920; PIDN:AAD25580.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g04890
A:Map position: 2
Query Match 20.4%; Score 564; DB 2; Length 413;
Best Local Similarity 34.1%; Pred. No. 2.6e-34;
Matches 133; Conservative 90; Mismatches 135; Indels 32; Gaps 14;
Qy 156 VVLVDSQENG-VRLVHALLACAEAVQKENLTVAEALVKQI-GFLAVSIGAMRKVATYFA 213

Db 39 LLIVEAISKGLKLV--LVACAKAVSENNLLMARCMGELRGWVSISG-EPIORLGAYML 95
Qy 214 EALARR-----IYRLSPSQPIDHS-LSDTLOMHFETCPYLKFAHFTANQAILFAQ 265
Db 96 EGLVARLAASGSIYKSLQSRPESEYEFLSYVYVLIH--EVCYFKEFGYMGANGAIAEAMK 153
Qy 266 GKRRVHVITDFSMOSQLOWPALMOALALRPGPPVPRLTGIGPPAPDNFDYLHEVGCKLAH 325
Db 154 DEERHIIDFQIGGQSOWIALIQAPARPAGGAPNTRITGVG-----DGSVLVTVKKRLEK 208
Qy 326 LAEATHVEFEYRGFVANTLADLASMLELRPSEIESVAVNSVFELHKL-----LGRPGAI 381
Db 209 LAKKFDVDFRENA-VSRPSCVEVENLDVRDG--EALGVNEFAYMLHLPDESVSVMENHRD 265
Qy 382 KVLGVVNOIKPEIFTVVEQSNHNSPIFLDRFTESLHYSTLFDLSLEGV--PSGQDKVMS 439
Db 266 RLLRNWKSLSKRVVTVLEQBCNTNTPFLPRFLTSLYTAMFESIDVMLPRNHKEIRINI 325
Qy 440 EYV-LGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAPKQAASMLLALFN 498
Db 326 EQHCWARDVNVLIACEGAERIERHELLGKWSRFSMAGFEPPPLSS--IISATIRALLRD 383
Qy 499 GEGYRVEESDGLMLGWHTRPLIATSAWK 528
Db 384 YSNGYAIERDGAFLYGMWDRILVSSCAWK 413
RESULT 10
E96542
scarecrow-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96542
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E96542
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-526 <STO>
A:Cross-references: GB:AE005173; NID:g11054625; PIDN:AAG27870.1; GSPDB:GN00141
C:Genetics:
A:Gene: F17J6.12
A:Map position: 1
Query Match 20.4%; Score 562.5; DB 2; Length 526;
Best Local Similarity 31.8%; Pred. No. 4.8e-34;
Matches 155; Conservative 86; Mismatches 180; Indels 67; Gaps 16;
Qy 60 QEDLSQLA-TETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNOFAIDSA 118
Db 87 EENNNSPLSGSSATNTNETLSLMLKDLLETAMPEPDVNSY----- 127
Qy 119 SSSNOGGGGDYTTNKRKLCNSGVVETTTATAESTRHVVLVDSQENGVRVLHALLACAEA 178
Db 128 --NNQGGFG-----QHGVV--SSAMYSMEMISRGD-----LKGVLTECAKA 166
Qy 179 VQENLTVAEALVKQIGFLAVSQICAMRKVATYFAEALARR-----IYRLSPSQSPID 231
Db 167 VENYDLENTDWLIISQLOQMVSVSGEPVORLGAYMLEGLVARLASSGSIYKALRCKDPTG 226
Qy 232 HSLSDTLOMH-FYETCPYLKFAHFTANQAILFAOGKKRVHVIDFMSQGLQWLPALMOAL 290

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Db      227 PEL--ITYWHILYEAQYPKFGYESANGAIAEAVKNSEFVHIIDFQISQGGQWVSLRAL 284
Qy      291 ALRPGGPPVFRITGIGPPAD--NFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLD 348
Db      285 GARGGPPNVRITGIDDPSSFAROGGLELVQRLGKLAEMCGVYFEFHG-AALCCTEVE 343
Qy      349 ASMLELRPSIEISVAVNSVFLHKLGRPGAI---DKVLGVNVQIKPEIFTVVVEQESNH 404
Db      344 IEKLGVRNG-EALAVNFPVLVHHMPDESVTVENHRDRLRLVKHLSPNVVTLVLEQEANT 401
Qy      405 NSPIFDRTESLHYSTLFDLSLEGVPSGD---KVISEVY-LGKQICNVVACDGPDRVE 460
Db      402 NTAPFLREFVETMNHYLAVFESID-VKLARDHKERINVEQCLAREVYNIACEGVVEREE 460
Qy      461 RHETLSQWRNRGSGAGFAAAHIGTNAFQASMLLALFNGEGYRVEESDCGLMLGWHTRP 520
Db      461 RHEPLGKWRSRHMGFKPYPLUSS--YVNATIKLLESYSEKYFTLEERDAGALYLGWKNOP 518
Qy      521 LIATSAAWK 528
Db      519 LITSAWR 526

RESULT 11
T51242
Sc11 protein [imported] - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C:Accession: T51242
R:Pysh, L.D.: Wyszocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N.
Plant J. 18, 111-119, 1999
A:title: The GRAS gene family in Arabidopsis: sequence characterization and
A:Reference number: Z25337; MUID:99272994
A:Accession: T51242
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <P>S>
A:Cross-references: EMBL:AF067400; PIDN:AAC98090.1
C:Genetics:
A:Gene: Sc11

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R:Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N. plant J. 18, 111-119, 1999
A:Title: The GRAS gene family in Arabidopsis: sequence characterization and basic exp
A:Reference number: 225337; MUID:99272994
A:Accession: T51236
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-306 <PYS>
A:Cross-references: EMBL:AF036302; PIDN:AAD24405.1
C:Genetics:
A:Gene: SCL5

Query Match 18.4%; Score 506.5; DB 2; Length 306;
Best Local Similarity 39.0%; Pred. No. 3.1e-30;
Matches 117; Conservative 58; Mismatches 108; Indels 17; Gaps 9;

Qy 240 MH-FYETCYLKAFTANQAIIAEFGKKRVHVIDFSMSQGLQWLPALMQALALRPGGPP 298
Db 13 MHILEACPYFAGYESANGATAEAVKNESFVHIIDFQISQGGQWVSLIRALGARGGPP 72
Qy 299 VFRLTGIGPPAD--NFDYLHEVGCKLAHAEAIHVEFYRGFVANTLADLASMLELRP 356
Db 73 NVKITGIDPRSSFARQGLELVGORLGLKAEMCGVPFEFHG-AALCCTEVEIEKLGVRN 131
Qy 357 SEIESVAVNSVELHKLGRPGAI----DKVLGVNVIQKPEIFTVVEQESHNSPIFLDR 412
Db 132 G-EALAVNPLVLVHMPDESVTVENHRDLRLVHLSPNVVTVLVEQEAINTAPFLLPR 189
Qy 413 FTESLHYSTLFDLSLEGVPSGD---KVMSEV-LGKOICNVVACDGDPRVERHETLSQW 468
Db 190 FVETMNHVLAVESID-VKLARDHKERINVEQHLAREVNVNLIACEGVEREERHEPLGKW 248
Qy 469 RNRFGSAGFAAAHIGSNAPKQASMLLALFNGGEGYRVESDGLCMLGMWHTPLIATSAMK 528
Db 249 RSRFHMGAKPYPLSS--YVNATIKGLLESYSEKYTEERDGLYLGWKNOPLITSCAWR 306

RESULT 13
E86347
hypothetical protein AAF87898.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
A:Accession: E86347
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: E86347
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-593 <STO>
A:Cross-references: GB:AE005172; NID:g9454575; PIDN:AAF87898.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

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Db 181 -EID-----SEWYQNEHQDQSPKESSAD-----SNGHVSSKEVVSQATPKQ 224
Qy 157 VLVDSEQNGVRLVHALLACAEAVOKENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEAL 216
Db 225 ILI-----SCARALSEGKLEALSWMNELRQIVSIQDPSQRIATAVMVEGL 270
Qy 217 ARR-----IYR-LSPSQSPIDHSDTLQMHFYETPCYLFKFAHFTANQALAEAFQKK 268
Db 271 AARMAASKGFIVYALKKEPPSDELA-AMQV-LFEVCPCKFGFLAANGAILEAIKGE 328
Qy 269 RVHVIDFSMSQGLQWALMALALPGGPPVRLTGICPP--APNFDYLHEVGCKLAHL 326
Db 329 EVHIIDFQINGQNTLTIRSAELPGRRRLRGLFGIDDPESVQRSIGGLRIIGRLLEQL 388
Qy 327 AEAIHVEYEGFVANTLADLADASMLELRPSIESVAVNSVFELHKL-----LGRPGADIK 382
Db 389 AEDNGSVKFKAMPKST-SIVSPSTLGCKPG--EFLIVNFAQLHMPHDESVTTVQNRDE 445
Qy 383 VLGVVNIQKPELFTVVEQSNHNSPIFLDRFTESLHYSTLFDLSLE-GVP-SGQDKV-MS 439
Db 446 LLHMVKSINPKLVTVEQDVNTNTSPFPFRTFAYEYISAVFESLDMTLPRESQERMNVE 505
Qy 440 EYVLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGS-----NAFKQASM 492
Db 506 ROCLARDIVNVACGEGERIERYEAGKWRARMMAAGFNPKPMSAKVTNNIQNLKQOYC 565
Qy 493 LLALFNGGEGYRVESDGLMLGWHTRPLIATSAWK 528
Db 566 -----NKYKKEEMGELHFCWEKSLIVASAWR 593

RESULT 14
T51232
scarecrow-like protein 14 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C:Accession: T51232
R:Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N.
Plant J. 18, 111-119, 1999
A:Title: The GRAS gene family in Arabidopsis: sequence characterization and basic expres
A:Reference number: 225337; MUID:99272994
A:Accession: T51232
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-808 <PYS>
A:Cross-references: EMBL:AF036309; PIDN:AAD24412.1
C:Genetics:
A:Gene: SCL14

Query Match 16.4%; Score 453.5; DB 2; Length 808;
Best Local Similarity 25.8%; Pred. No. 1.2e-25;
Matches 151; Conservative 91; Mismatches 185; Indels 159; Gaps 21;

Qy 4 DHHHHQ-----DKTKMMNEEDGNGMDELLAVLYGKYKRSSEMADVAQKLEQEV 54
Db 325 EHHHHVSAPPNRLTGKKSHWRDEDE-----FVEERSNKQSAV----- 364

Qy 55 MMSNVQEDDLSQLATEVTHYNPAELYTWLDSMLTDLPSPSSNAEYDLKAIFGD--AIIHQ 112
Db 365 ---YVEESELSEM-----FDNMF-----CGFGKPCVILNQ 392

Qy 113 -FADSSASSNGGGDPTTNTKRLKCSNGVVETTATAESTRHVVLVDSOENGVRVLA 171
Db 393 NFPTESAKVTVAQNGAKIRGK-----STSTSHN-----DSKKTADRTL 435

Qy 172 LLACAEAVOKENLVAEALVKQIGFLAVSQIGAMRKVATYFAEALARR-----IYRLS 224
Db 436 LVLCQAQVSVDRRTANEMLRQIREHSSPLNGSERLAHYFANSLEARLAGTGQIYAL 495

Qy 225 PSQSPIDHSLDSTLQMH--FYETPCYLFKFAHFTANQALAEAFQKKRVHVIDFSMSQGLQ 282
Db 225 PSQSPIDHSLDSTLQMH--FYETPCYLFKFAHFTANQALAEAFQKKRVHVIDFSMSQGLQ 282
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Db 496 SSKKT---SAADMLKAYQTYMSVCPFKKAAIIFANHSMRFTANANTIIHIDFISYGFQ 552
Qy 283 WPALMQALAL-RPGGPPVRLTGIGPPAPDNFDYLHEVGCKLAHLAEALHVEFEYRGF-- 339
Db 553 WPALHRLSLSPGSGPKLRITGI-----ELPQGRFP 585
Qy 340 -----VANTLADLADASML-----ELRPSIESVAVNSVFELHKLIG 375
Db 586 AEEFRQVIAWLDVSTDMFRLSTTQLNRGETIQVEDLKLQGEYVVVNSLFRNLLD 645
Qy 376 RPGAI----DKVLGVVNIQKPELFTVVEQSNHNSPIFLDRFTESLHYSTLFDLSLEGPV 431
Db 646 ETVLNSPRDAVLKLRKINPNVFIPTALSGYNAPFFVREFREALFHSYAVDFMCDCKL 705
Qy 432 SGQDKV----MSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAF 487
Db 706 AREDEMRLMYFEFY-GREIVNVASEGTERVESRETQWQARLIRAGFQLPLEKELM 764
Qy 488 KOASMLLALFNG-GEYRVESDGLMLGWHTRPLIATSAWKLN 532
Db 765 Q--NLKLIENGYDKNFQDQNGNLLQGWKGRIVYASSLWVPSS 808

RESULT 15
T51234
scarecrow-like protein 1 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C:Accession: T51234
R:Pysh, L.D.; Wysocka-Diller, J.W.; Camilleri, C.; Bouchez, D.; Benfey, P.N.
Plant J. 18, 111-119, 1999
A:Title: The GRAS gene family in Arabidopsis: sequence characterization and basic expres
A:Reference number: 225337; MUID:99272994
A:Accession: T51234
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <PYS>
A:Cross-references: EMBL:AF036300; PIDN:AAD24403.1
C:Genetics:
A:Gene: SCL1

Query Match 16.4%; Score 451.5; DB 2; Length 352;
Best Local Similarity 32.7%; Pred. No. 4.9e-26;
Matches 119; Conservative 70; Mismatches 138; Indels 37; Gaps 13;

Qy 189 ALVKQIGFLAVSQIGAMRKVATYFAEALARR-----IYR-LSPSQSPIDHSLDSTLQ 240
Db 2 SMVNELQIVSIQDPSQRIATAVMVEGLAARMAASGKFIYALKCKEPPSDELA-AMQV 60

Qy 241 HFYETCPYLKFAHFTANQALAEAFQKKRVHVIDFSMSQGLQWALMALALRPGGPPV 300
Db 61 -LFEVCPCKFGFLAANGAILEAIKGEVEHIIIDFQINGQNYMTLIRISIAELPKRRPL 119

Qy 301 RLGTGIGPP--APDNFDYLHEVGCKLAHLAEALHVEFEYRGFVANTLADLADASMLELRPSE 358
Db 120 RLGTGIDDPESVORSIGGLRIIGRLQLEADENGVSFKFKAMPKST-SIVSPSTLGCKPG- 177

Qy 359 IESVAVNSVFELHKL-----LGRPGADIKVLGVVNIQKPELFTVVEQSNHNSPIFLDRFT 414
Db 178 -ETLVNFAFOLHHPDESVTNNQORDELLHVMKSLNPKLVTVEQDVNTNTSPFPFRI 236

Qy 415 ESLHYSTLFDLSLE-GVP-SGQDKV-MSEVYLGKQICNVVACDGPDRVERHETLSQWRN 471
Db 237 EAYEYISAVFESLDMTLPRESQERMNVERQCLARDIVNVACGEGERIERYEAGKWRAR 296

Qy 472 FGSAGFAAAHIGS-----NAFKQASMLLALFNGGEGYRVESDGLMLGWHTRPLIAT 524
Db 297 MMAGFNPKPSAKVTNNIQNLKQOYC-----NKYKKEEMGELHFCWEKSLIVA 348

Qy 525 SAWK 528
Db 349 SAWR 352
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Job time: 209 sec
